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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: Wed Sep 05 15:35:32 EDT 2007

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Reviewer Comments:

<210> 6

<211> 6

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<213> Homo sapiens

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<221> Variant

<222> (1)..(1)

<223> Wherein Xaa is an N-acetyl group.

<220>

<221> Variant

<222> (6)..(6)

<223> Wherein Xaa is a 7-amino-4-methylcoumarin group.

<400> 6

Xaa Ile Glu Pro Asp Xaa

1 5

The above explanations for Xaa are invalid: "Xaa" can only represent a single amino acid, not a functional group.

<210> 29

<211> 4

<212> PRT

<213> Homo sapiens

<220>
<223> Chymotrypsin substrate specificity

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Xaa Xaa Xaa Xaa
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The above <223> explanation for "Xaa" at location 4 contains a misspelling: please replace "ot" with "or."

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<400> 54
Xaa Xaa Leu Xaa
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The above "<222> 3" is an incorrect location for "Xaa:" "Leu" is at location 3; "Xaa" is at location 2.

Application No: 10677977 Version No: 4.0

Input Set:

Output Set:

Started: 2007-08-23 14:48:11.063
Finished: 2007-08-23 14:48:11.915
Elapsed: 0 hr(s) 0 min(s) 0 sec(s) 852 ms
Total Warnings: 3
Total Errors: 3
No. of SeqIDs Defined: 57
Actual SeqID Count: 57

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (3)
W 213	Artificial or Unknown found in <213> in SEQ ID (5)
W 213	Artificial or Unknown found in <213> in SEQ ID (22)
E 257	Invalid sequence data feature in <221> in SEQ ID (22)
E 257	Invalid sequence data feature in <221> in SEQ ID (22)
E 341	'Xaa' position not defined SEQID (54) POS (2)

SEQUENCE LISTING

<110> Nguyen, Jack
 Thanos, Chris
 Waugh Ruggles, Sandra
 Craik, Charles S.

<120> METHODS OF GENERATING AND SCREENING FOR PROTEASES WITH ALTERED
 SPECIFICITY

<130> 19049-005001/4905

<140> 10677977
 <141> 2003-10-02

<150> 60/425,388
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Leu	Asp	Asn	Ser	Tyr	Lys	Met	Asp	Tyr	Pro	Glu	Met	Gly	Leu	Cys	Ile
		35					40					45			

Ile	Ile	Asn	Asn	Lys	Asn	Phe	His	Lys	Ser	Thr	Gly	Met	Thr	Ser	Arg
50						55					60				

Ser	Gly	Thr	Asp	Val	Asp	Ala	Ala	Asn	Leu	Arg	Glu	Thr	Phe	Arg	Asn
65					70					75					80

Leu	Lys	Tyr	Glu	Val	Arg	Asn	Lys	Asn	Asp	Leu	Thr	Arg	Glu	Glu	Ile
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Val	Glu	Leu	Met	Arg	Asp	Val	Ser	Lys	Glu	Asp	His	Ser	Lys	Arg	Ser
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Ser Phe Val Cys Val Leu Leu Ser His Gly Glu Glu Gly Ile Ile Phe
115 120 125

Gly Thr Asn Gly Pro Val Asp Leu Lys Lys Ile Thr Asn Phe Phe Arg
130 135 140

Gly Asp Arg Cys Arg Ser Leu Thr Gly Lys Pro Lys Leu Phe Ile Ile
145 150 155 160

Gln Ala Cys Arg Gly Thr Glu Leu Asp Cys Gly Ile Glu Thr Asp Ser
165 170 175

Gly Val Asp Asp Asp Met Ala Cys His Lys Ile Pro Val Asp Ala Asp
180 185 190

Phe Leu Tyr Ala Tyr Ser Thr Ala Pro Gly Tyr Tyr Ser Trp Arg Asn
195 200 205

Ser Lys Asp Gly Ser Trp Phe Ile Gln Ser Leu Cys Ala Met Leu Lys
210 215 220

Gln Tyr Ala Asp Lys Leu Glu Phe Met His Ile Leu Thr Arg Val Asn
225 230 235 240

Arg Lys Val Ala Thr Glu Phe Glu Ser Phe Ser Phe Asp Ala Thr Phe
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Leu Tyr Phe Tyr His
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Xaa Xaa Leu Xaa

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<223> Xaa=Val, Phe or Tyr

<220>
<221> VARIANT
<222> 4
<223> Xaa=Arg or Lys

<400> 56
Xaa Xaa Xaa Xaa
1

<210> 57
<211> 4
<212> PRT
<213> Homo sapiens

<220>
<223> Cruzain substrate spec.

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